



PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Boo

Search for

Limits

Preview/Index

History

Clipboard

Details

Display

Show:

Send to

1: [AL136644](#). Homo sapiens mRNA...[gi:12052813][Links](#)

LOCUS HSM800069 636 bp mRNA linear PRI 05-JAN-2001

DEFINITION Homo sapiens mRNA; cDNA DKFZp564M173 (from clone DKFZp564M173); complete cds.

ACCESSION AL136644

VERSION AL136644.1 GI:12052813

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 636)

AUTHORS Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S.

TITLE Direct Submission

JOURNAL Submitted (18-JAN-2000) MIPS, Am Klopferspitz 18a, D-82152 Martinsried, GERMANY

COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at <http://www.mips.biochem.mpg.de/proj/cDNA/>.

FEATURES

source Location/Qualifiers

1..636

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp564M173"

/tissue_type="brain"

/clone_lib="564 (synonym: hfbr2). Vector pAMP1; host Xl-2blue; sites NotI + SalI"

/dev_stage="fetal"

gene 26..403

/gene="DKFZp564M173"

CDS 26..403

/gene="DKFZp564M173"

/note="similarity to Drosophila janus A"

/codon_start=1

/product="hypothetical protein"

/protein_id="CAB66579.1"

/db_xref="GI:12052814"

/translation="MAVADLALIPDVDTSDSGVFKYVLIRIHSAPRSGAPAAESKEIV RGYKWAHEYHADIYDKVSGDMQKQGCDCECLGGGRTSHQSQDKKIHVYGYSMAYGPAQH AISTEKIKAKYPDYEVTWANDGY"

polyA_signal 561..566

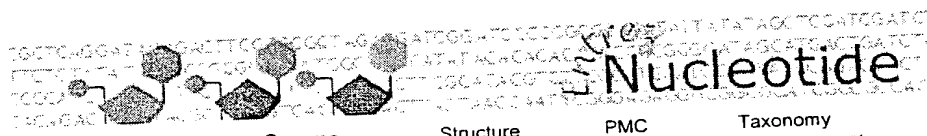
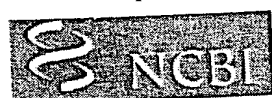
polyA_site 575

BASE COUNT 176 a 184 c 172 g 104 t
ORIGIN
1 gaaggggggac tccgggagga ggaacatggc ggtggcggac ctcgctctca ttctgatgt
61 ggacaccgac tccgacggcg tcttcaagta tgtgctgac cgaatccact cggctccccg
121 ctccggggct ccggctgcag agagcaagga gatcgtgcgc ggctacaagt gggctgagta
181 ccatgctggac atctacgaca aagtgtcggg cgacatgcag aagcaaggct gcgactgtga
241 gtgtctgggc ggcgggcgca cctcccacca gagtcaggac aagaagattc acgtgtacgg
301 ctattccatg gcctatggtc ctgcccagca cgccatttca actgagaaaa tcaaagccaa
361 gtaccccgac tacgaggtca cctgggctaa cgacggctac tgagcactcc cagcccgggg
421 cctgctgect ccagcagcca cttcagagcc cccgcctttg cctgcactcc tcttgcaggg
481 ctggccctgc ctgctcctgc ggcagcctct ggtgacgtgc tgtccaccag gccttggaga
541 caggctagcc tggccacaga attaaacgtg ttgccacaaa aaaaaaaaaa aaaaaaaaaa
601 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Sep 16 2003 13:15:10

NCBI Sequence Viewer



Search for

Links

☐ 1: AL136644. Homo sapiens mRNA...[gi:12052813]

LOCUS HSM800069 636 bp mRNA linear PRI 12-JUL-2002
 DEFINITION Homo sapiens mRNA; cDNA DKFZp564M173 (from clone DKFZp564M173); complete cds.
 ACCESSION AL136644
 VERSION AL136644.1 GI:12052813
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 636)
 AUTHORS Wambutt, R., Heubner, D., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
 TITLE Direct Submission
 JOURNAL Submitted (10-JUL-2002) GSF, Institut fuer Bioinformatik MIPS, Ingolstaedter Landstr. 1, 85764 Neuherberg, Germany
 COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
 This clone (DKFZp564M173) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at <http://mips.gsf.de/proj/cDNA/>.
 FEATURES
 source Location/Qualifiers
 1..636
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="9"
 /clone="DKFZp564M173"
 /tissue_type="brain"
 /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host X1-2blue; sites NotI + Sali"
 /dev_stage="fetal"
 gene 1..636
 /gene="DKFZp564M173"
 CDS 26..403
 /gene="DKFZp564M173"
 /note="similarity to Drosophila janus A"
 /codon_start=1
 /product="hypothetical protein"
 /protein_id="CAB66579.1"
 /db_xref="GI:12052814"
 /db_xref="SPTREMBL:Q9H0Y3"
 /translation="MAVADLALIPDVTDSGDGVFKYVLIRIHSAPRSGAPAAESKEIV RGYKWAHEYHADIYDKVSGDMQKQGCDCLEGGRTSHQSQDKIHVYGYSMAYGPAQH AISTEKIKAKYPDYEVTWANDGY"
 polyA signal 561..566
 /gene="DKFZp564M173"

CBI Sequence Viewer

polyA site 575
 /gene="DKFZp564M173"
 ASE COUNT 176 a 184 c 172 g 104 t

RIGIN
 1 gaaggggggac tccggggagga ggaacatggc ggtggcggac ctgctctca ttcctgatgt
 61 ggacaccgac tccgacggcg tcttcaagta tgtgctgatc cgaatccact cggctccccg
 121 ctccgggggt cggctgcag agagcaagga gatcgtgcgc ggctacaagt gggctgagta
 181 ccatgcggac atctacgaca aagtgtcggg cgacatgcag aagcaaggct gcgactgtga
 241 gtgtctgggc ggcgggcgca cctcccacca ggtcaggac aagaagattc acgtgtacgg
 301 ctattccatg gcctatggtc ctgcccagca cgccatttca actgagaaaa tcaaagccaa
 361 gtaccccgac tacgaggtca cctgggctaa cgacggctac tgagcactcc cagcccgggg
 421 cctgctgcct ccagcagcca cttcagagcc cccgcctttg cctgcactcc tcttgcaggg
 481 ctggccctgc ctgctcctgc ggcagcctct ggtgacgtgc tgtccaccag gccttggaga
 541 caggctagcc tggccacaga attaaacgtg ttgccacaaa aaaaaaaaaa aaaaaaaaaa
 601 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa

//

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

Jul 8 2003 12:22:35

RID=1058466116-018697-25282,



results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1058466116-018697-25282

Query=

(125 letters)

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF

1,472,278 sequences; 474,667,288 total letters

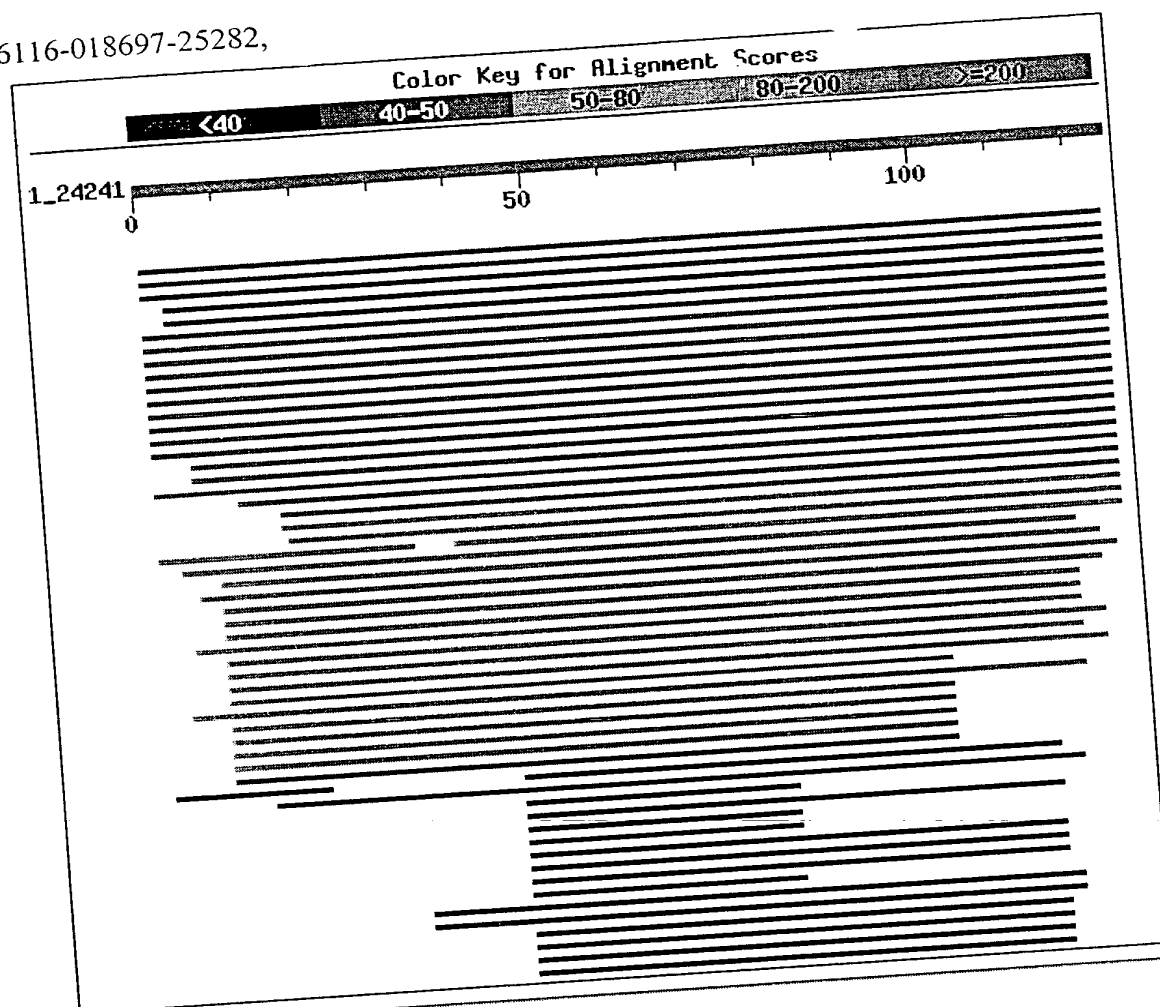
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 72 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments

RID=1058466116-018697-25282,



Sequences producing significant alignments:

	Score (bits)	E Value	
gi 24475861 ref NP_054891.2 phosphohistidine phosphatase; ...	239	4e-63	L
gi 12052814 emb CAB66579.1 hypothetical protein [Homo sapi...	236	5e-62	L
gi 32363249 sp P83468 PHP1 RABIT 14 kDa phosphohistidine ph...	204	2e-52	
gi 27706196 ref XP_216013.1 similar to RIKEN cDNA 1700008C...	201	2e-51	L
gi 25021092 ref XP_203853.1 RIKEN cDNA 1700008C22 [Mus mus...	201	2e-51	L
gi 31241091 ref XP_320969.1 ENSANGP00000019900 [Anopheles ...	108	2e-23	
gi 1708582 sp P54364 JANA DROPS Sex-regulated protein janus...	105	2e-22	
gi 1362647 pir S53876 sex-regulated protein janus A - frui...	100	3e-21	
gi 12408210 gb AAG50362.1 janusA [Drosophila yakuba] >gi 1...	95	2e-19	
gi 28572013 ref NP_788762.1 janus A CG7933-PB [Drosophila ...	93	6e-19	L
gi 12408214 gb AAG50364.1 janusA [Drosophila erecta]	93	8e-19	
gi 12408216 gb AAG50365.1 janusA [Drosophila orena]	93	8e-19	
gi 12408208 gb AAG50361.1 janusA [Drosophila mauritiana]	92	2e-18	
gi 32565108 ref NP_492382.2 Janus/Ocnus (13.2 kD) (1J389) ...	91	2e-18	
gi 12408206 gb AAG50360.1 janusA [Drosophila simulans] >gi...	91	2e-18	
gi 28572011 ref NP_788763.1 janus A CG7933-PA [Drosophila ...	91	3e-18	L
gi 14669708 gb AAK72008.1 AF393330 1 janusA [Drosophila sim...	91	3e-18	
gi 19527887 gb AAL90058.1 AT12574p [Drosophila melanogaster]	89	9e-18	L
gi 12239449 gb AAG49478.1 janus A [Drosophila sechellia]	82	2e-15	
gi 12239431 gb AAG49466.1 janus A [Drosophila simulans]	82	2e-15	
gi 12239440 gb AAG49472.1 janus A [Drosophila mauritiana]	79	1e-14	
gi 12239434 gb AAG49468.1 janus A [Drosophila simulans] >g...	78	2e-14	

<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

RID=1058466116-018697-25282,

gi 6841504 gb AAF29105.1 AF161490.1	HSPC141 [Homo sapiens]	74	3e-13
gi 7500587 pir T21833	hypothetical protein F36A2.8 - Caeno...	71	3e-12
gi 1708583 sp P54365 JANB DROPS	Sex-regulated protein janus...	60	5e-09
gi 12408242 gb AAG50371.1	janusB [Drosophila erecta]	59	2e-08
gi 24582967 ref NP_652561.1	CG18662-PA [Drosophila melanog...	58	3e-08
gi 12408240 gb AAG50370.1	janusB [Drosophila teissieri]	57	4e-08
gi 125062 sp P20349 JANB DROME	Sex-regulated protein janus-...	57	5e-08
gi 12408234 gb AAG50367.1	janusB [Drosophila sechellia]	57	5e-08
gi 12408232 gb AAG50366.1	janusB [Drosophila simulans] >gi...	57	7e-08
gi 12408238 gb AAG50369.1	janusB [Drosophila yakuba]	56	1e-07
gi 12408236 gb AAG50368.1	janusB [Drosophila mauritiana]	56	1e-07
gi 12408244 gb AAG50372.1	janusB [Drosophila orena]	55	1e-07
gi 12408230 gb AAG50379.1	ocnus [Drosophila orena]	54	4e-07
gi 1362648 pir S53877	sex-regulated protein janus B - frui...	54	5e-07
gi 12408224 gb AAG50376.1	ocnus [Drosophila yakuba] >gi 12...	52	1e-06
gi 12408222 gb AAG50375.1	ocnus [Drosophila mauritiana]	51	3e-06
gi 17864098 ref NP_524578.1	ocnus CG7929-PA [Drosophila me...	51	3e-06
gi 12408218 gb AAG50373.1	ocnus [Drosophila simulans] >gi ...	51	3e-06
gi 12408228 gb AAG50378.1	ocnus [Drosophila erecta]	43	8e-04
gi 25008915 sp P59083.1	[Segment 1 of 4] 14 kDa phosphohis...	37	0.058
gi 19569973 gb AAL92276.1	hypothetical protein [Dictyostel...	33	0.64
gi 6934223 gb AAF31658.1 AF162079.1	beta-tubulin 1 [Harpoch...	33	0.85
gi 30088584 gb AAN35158.1	beta-tubulin [Nowakowskiella ele...	33	0.95
gi 13649518 gb AAK37434.1 AF267183.1	beta-tubulin [Jakoba i...	31	3.5
gi 7441373 pir S35191	tubulin beta-1 chain - fungus (Trich...	31	3.6
gi 401163 sp P31864 TBB1 TRIVI	TUBULIN BETA-1 CHAIN >gi 520...	31	3.6
gi 1096761 prf I2112315A	tubulin:SUBUNIT=beta	31	3.7
gi 20140402 sp Q9N2N6 TBB EUPFO	Tubulin beta chain (Beta-tu...	31	4.8
gi 26450912 dbj BAC42563.1	putative tubulin beta-6 chain [...	30	5.3
gi 28557457 gb AAO17775.1	beta-tubulin 1 [Hypocrea virens]	30	5.4
gi 4105829 gb AAD02570.1	nuclear beta-tubulin [Guillardia ...	30	5.4
gi 4105831 gb AAD02571.1	nuclear beta-tubulin [Guillardia ...	30	7.1
gi 8928411 sp Q39697 TBB2 DAUCA	Tubulin beta-2 chain (Beta-...	30	7.6
gi 18157542 dbj BAB83857.1	beta tubulin-partially supporte...	30	7.9
gi 13649531 gb AAK37438.1 AF267187.1	beta-tubulin [Reclinom...	30	7.9
gi 13649541 gb AAK37440.1 AF267189.1	beta-tubulin [Reclinom...	30	7.9
gi 13649546 gb AAK37441.1 AF267190.1	beta-tubulin [Reclinom...	30	7.9
gi 13649533 gb AAK37439.1 AF267188.1	beta-tubulin [Reclinom...	30	8.0
gi 13649522 gb AAK37435.1 AF267184.1	beta-tubulin [Jakoba l...	30	8.1
gi 16215677 emb CAC95049.1	subtilisin-like serine protease...	30	8.1
gi 117631 sp P29138 CUDP METAN	Cuticle-degrading protease p...	30	8.4
gi 5901587 gb AAD55354.1 AF119173.1	beta-tubulin [Cercomona...	30	8.6
gi 1729844 sp P50260 TBB2 PORPU	TUBULIN BETA-2 CHAIN >gi 10...	30	9.0
gi 181816 pir JA0048	tubulin beta-1 chain - soybean	30	9.0
gi 14331109 emb CAC40860.1	beta-tubulin [Medicago sativa s...	30	9.0
gi 135452 sp P12459 TBB1 SOYBN	TUBULIN BETA-1 CHAIN >gi 170...	30	9.2
gi 5733382 gb AAD49555.1 AF095840.1	b-tubulin [Entosiphon s...	30	9.3
gi 13661265 gb AAK37834.1 AF182558.1	beta-tubulin [Euglena ...	30	9.3
gi 135475 sp P20802 TBB ACHKL	TUBULIN BETA CHAIN >gi 100989...	30	9.3
gi 6094432 sp O59837 TBB PHYCI	TUBULIN BETA CHAIN >gi 29519...	30	9.5

Alignments

☐ >gi|24475861|ref|NP_054891.2| sapiens] ☒ phosphohistidine phosphatase; sex-regulated p
 gi|25008934|sp|Q9NRX4|PHP1 HUMAN ☒ 14 kDa phosphohistidine phosphatase (Protein
<http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

RID=1058466116-018697-25282,

(HSPC141) (CGI-202) ☒ sex-regulated protein janus-a [Homo sapiens]
gi|8895093|gb|AAF80759.1|AF164795.1 ☒ CGI-202 [Homo sapiens]
gi|9858829|gb|AAG01156.1|AF285119.1 ☒ Similar to HSPC141 protein [Homo sapiens]
gi|19353100|gb|AAH24648.1| ☒ phosphohistidine phosphatase [Homo sapiens]
gi|24306046|gb|AAN52504.1|AF393504.1
Length = 125

Score = 239 bits (611), Expect = 4e-63
Identities = 125/125 (100%), Positives = 125/125 (100%)

Query: 1 MAVADLALIPDVIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGYKWAHEYHADIYDKV 60
MAVADLALIPDVIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGYKWAHEYHADIYDKV
Sbjct: 1 MAVADLALIPDVIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGYKWAHEYHADIYDKV 60
Query: 61 SGDMQKQGCDCECLGGGRISHQSQDKKIHVYGYSMAYGPAQHAISTEKIKAKYPDYEVTW 120
SGDMQKQGCDCECLGGGRISHQSQDKKIHVYGYSMAYGPAQHAISTEKIKAKYPDYEVTW
Sbjct: 61 SGDMQKQGCDCECLGGGRISHQSQDKKIHVYGYSMAYGPAQHAISTEKIKAKYPDYEVTW 120
Query: 121 ANDGY 125
ANDGY
Sbjct: 121 ANDGY 125

☐ >gi|12052814|emb|CAB66579.1| ☒ hypothetical protein [Homo sapiens]
Length = 125

Score = 236 bits (602), Expect = 5e-62
Identities = 122/125 (97%), Positives = 123/125 (98%)

Query: 1 MAVADLALIPDVIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGYKWAHEYHADIYDKV 60
MAVADLALIPDVIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGYKWAHEYHADIYDKV
Sbjct: 1 MAVADLALIPDVIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGYKWAHEYHADIYDKV 60
Query: 61 SGDMQKQGCDCECLGGGRISHQSQDKKIHVYGYSMAYGPAQHAISTEKIKAKYPDYEVTW 120
SGDMQKQGCDCECLGGGRISHQSQDKKIHVYGYSMAYGPAQHAISTEKIKAKYPDYEVTW
Sbjct: 61 SGDMQKQGCDCECLGGGRISHQSQDKKIHVYGYSMAYGPAQHAISTEKIKAKYPDYEVTW 120
Query: 121 ANDGY 125
ANDGY
Sbjct: 121 ANDGY 125

☐ >gi|32363249|sp|P83468|PHP1 RABIT 14 kDa phosphohistidine phosphatase (Protein h
(PHP)
Length = 125

Score = 204 bits (519), Expect = 2e-52
Identities = 105/125 (84%), Positives = 115/125 (92%)

Query: 1 MAVADLALIPDVIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGYKWAHEYHADIYDKV 60
MA A LA IPDVIDSDGVFKYVLIRVH+AP S AP ESK+IVRGYKWAHEYHADIYDKV
Sbjct: 1 MAAAGLAQIPDVIDSDGVFKYVLIRVHAAPPSEAPGGESKDIVRGYKWAHEYHADIYDKV 60
Query: 61 SGDMQKQGCDCECLGGGRISHQSQDKKIHVYGYSMAYGPAQHAISTEKIKAKYPDYEVTW 120
SG++QK+G DCECLGGGRISHQSQDKKIHVYGYSM YG AQH++STEKI+AKYPDYEVTW
Sbjct: 61 SGELQKKGHDCECLGGGRISHQSQDKKIHVYGYSMGYGRAQHSVSTEKIRAKYPDYEVTW 120
Query: 121 ANDGY 125
A+DGY